



✓ 36

SEQUENCE LISTING

<110> Voellmy, Richard

<120> MOLECULAR REGULATORY CIRCUITS TO ACHIEVE
SUSTAINED ACTIVATION OF GENES OF INTEREST BY A SINGLE STRESS

<130> 870109.409

<140> US 09/304,121

<141> 1999-05-03

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<212> DNA

<213> Homo sapien

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tttgcgggcg ctccctccgc ctattccctc cttgctcgag atg gat ctg ccc gtg      175
                                     Met Asp Leu Pro Val
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ggc ccc ggc gcg gcg ggg ccc agc aac gtc ccg gcc ttc ctg acc aag      223
Gly Pro Gly Ala Ala Gly Pro Ser Asn Val Pro Ala Phe Leu Thr Lys
                                     10           15           20

ctg tgg acc ctc gtg agc gac ccg gac acc gac gcg ctc atc tgc tgg      271
Leu Trp Thr Leu Val Ser Asp Pro Asp Thr Asp Ala Leu Ile Cys Trp
                                     25           30           35

agc ccg agc ggg aac agc ttc cac gtg ttc gac cag ggc cag ttt gcc      319
Ser Pro Ser Gly Asn Ser Phe His Val Phe Asp Gln Gly Gln Phe Ala
                                     40           45           50

aag gag gtg ctg ccc aag tac ttc aag cac aac aac atg gcc agc ttc      367
Lys Glu Val Leu Pro Lys Tyr Phe Lys His Asn Asn Met Ala Ser Phe
                                     55           60           65

gtg cgg cag ctc aac atg tat ggc ttc cgg aaa gtg gtc cac atc gag      415
Val Arg Gln Leu Asn Met Tyr Gly Phe Arg Lys Val Val His Ile Glu
                                     70           75           80

cag ggc ggc ctg gtc aag cca gag aga gac gac acg gag ttc cag cac      463
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237

Gln	Gly	Gly	Leu	Val	Lys	Pro	Glu	Arg	Asp	Asp	Thr	Glu	Phe	Gln	His		
				90					95					100			
cca	tgc	ttc	ctg	cgt	ggc	cag	gag	cag	ctc	ctt	gag	aac	atc	aag	agg	511	
Pro	Cys	Phe	Leu	Arg	Gly	Gln	Glu	Gln	Leu	Leu	Glu	Asn	Ile	Lys	Arg		
			105					110					115				
aaa	gtg	acc	agt	gtg	tcc	acc	ctg	aag	agt	gaa	gac	ata	aag	atc	cgc	559	
Lys	Val	Thr	Ser	Val	Ser	Thr	Leu	Lys	Ser	Glu	Asp	Ile	Lys	Ile	Arg		
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cag	gac	agc	gtc	acc	aag	ctg	ctg	acg	gac	gtg	cag	ctg	atg	aag	ggg	607	
Gln	Asp	Ser	Val	Thr	Lys	Leu	Leu	Thr	Asp	Val	Gln	Leu	Met	Lys	Gly		
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aag	cag	gag	tgc	atg	gac	tcc	aag	ctc	ctg	gcc	atg	aag	cat	gag	aat	655	
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Glu	Ala	Leu	Trp	Arg	Glu	Val	Ala	Ser	Leu	Arg	Gln	Lys	His	Ala	Gln		
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caa	cag	aaa	gtc	gtc	aac	aag	ctc	att	cag	ttc	ctg	atc	tca	ctg	gtg	751	
Gln	Gln	Lys	Val	Val	Asn	Lys	Leu	Ile	Gln	Phe	Leu	Ile	Ser	Leu	Val		
			185				190						195				
cag	tca	aac	cgg	atc	ctg	ggg	gtg	aag	aga	aag	atc	ccc	ctg	atg	ctg	799	
Gln	Ser	Asn	Arg	Ile	Leu	Gly	Val	Lys	Arg	Lys	Ile	Pro	Leu	Met	Leu		
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aac	gac	agt	ggc	tca	gca	cat	tcc	atg	ccc	aag	tat	agc	cgg	cag	ttc	847	
Asn	Asp	Ser	Gly	Ser	Ala	His	Ser	Met	Pro	Lys	Tyr	Ser	Arg	Gln	Phe		
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tcc	ctg	gag	cac	gtc	cac	ggc	tcg	ggc	ccc	tac	tcg	gcc	ccc	tcc	cca	895	
Ser	Leu	Glu	His	Val	His	Gly	Ser	Gly	Pro	Tyr	Ser	Ala	Pro	Ser	Pro		
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Ala	Tyr	Ser	Ser	Ser	Ser	Leu	Tyr	Ala	Pro	Asp	Ala	Val	Ala	Ser	Ser		
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gga	ccc	atc	atc	tcc	gac	atc	acc	gag	ctg	gct	cct	gcc	agc	ccc	atg	991	
Gly	Pro	Ile	Ile	Ser	Asp	Ile	Thr	Glu	Leu	Ala	Pro	Ala	Ser	Pro	Met		
			265				270					275					
gcc	tcc	ccc	ggc	ggg	agc	ata	gac	gag	agg	ccc	cta	tcc	agc	agc	ccc	1039	
Ala	Ser	Pro	Gly	Gly	Ser	Ile	Asp	Glu	Arg	Pro	Leu	Ser	Ser	Ser	Pro		
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ctg	gtg	cgt	gtc	aag	gag	gag	ccc	ccc	agc	ccg	cct	cag	agc	ccc	cgg	1087	
Leu	Val	Arg	Val	Lys	Glu	Glu	Pro	Pro	Ser	Pro	Pro	Gln	Ser	Pro	Arg		
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338

gta gag gag gcg agt ccc ggg cgc cca tct tcc gtg gac acc ctc ttg	1135
Val Glu Glu Ala Ser Pro Gly Arg Pro Ser Ser Val Asp Thr Leu Leu	
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Ser Pro Thr Ala Leu Ile Asp Ser Ile Leu Arg Glu Ser Glu Pro Ala	
330 335 340	
ccc gcc tcc gtc aca gcc ctc acg gac gcc agg ggc cac acg gac acc	1231
Pro Ala Ser Val Thr Ala Leu Thr Asp Ala Arg Gly His Thr Asp Thr	
345 350 355	
gag ggc cgg cct ccc tcc ccc ccg ccc acc tcc acc cct gaa aag tgc	1279
Glu Gly Arg Pro Pro Ser Pro Pro Pro Thr Ser Thr Pro Glu Lys Cys	
360 365 370	
ctc agc gta gcc tgc ctg gac aag aat gag ctc agt gac cac ttg gat	1327
Leu Ser Val Ala Cys Leu Asp Lys Asn Glu Leu Ser Asp His Leu Asp	
375 380 385	
gct atg gac tcc aac ctg gat aac ctg cag acc atg ctg agc agc cac	1375
Ala Met Asp Ser Asn Leu Asp Asn Leu Gln Thr Met Leu Ser Ser His	
390 395 400 405	
ggc ttc agc gtg gac acc agt gcc ctg ctg gac ctg ttc agc ccc tcg	1423
Gly Phe Ser Val Asp Thr Ser Ala Leu Leu Asp Leu Phe Ser Pro Ser	
410 415 420	
gtg acc gtg ccc gac atg agc ctg cct gac ctt gac agc agc ctg gcc	1471
Val Thr Val Pro Asp Met Ser Leu Pro Asp Leu Asp Ser Leu Ala	
425 430 435	
agt atc caa gag ctc ctg tct ccc cag gag ccc ccc agg cct ccc gag	1519
Ser Ile Gln Glu Leu Leu Ser Pro Gln Glu Pro Pro Arg Pro Pro Glu	
440 445 450	
gca gag aac agc agc ccg gat tca ggg aag cag ctg gtg cac tac aca	1567
Ala Glu Asn Ser Ser Pro Asp Ser Gly Lys Gln Leu Val His Tyr Thr	
455 460 465	
gcg cag ccg ctg ttc ctg ctg gac ccc ggc tcc gtg gac acc ggg agc	1615
Ala Gln Pro Leu Phe Leu Leu Asp Pro Gly Ser Val Asp Thr Gly Ser	
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aac gac ctg ccg gtg ctg ttt gag ctg gga gag ggc tcc tac ttc tcc	1663
Asn Asp Leu Pro Val Leu Phe Glu Leu Gly Glu Gly Ser Tyr Phe Ser	
490 495 500	
gaa ggg gac ggc ttc gcc gag gac ccc acc atc tcc ctg ctg aca ggc	1711
Glu Gly Asp Gly Phe Ala Glu Asp Pro Thr Ile Ser Leu Leu Thr Gly	
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Ser Glu Pro Pro Lys Ala Lys Asp Pro Thr Val Ser	
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39

439

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tgcaggttgt tcatagtcag aattgtattt tggattttta cacaactgtc ccgttccccg 2057
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Val	Val	His	Ile	Glu	Gln	Gly	Gly	Leu	Val	Lys	Pro	Glu	Arg	Asp	Asp
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Glu	Asn	Ile	Lys	Arg	Lys	Val	Thr	Ser	Val	Ser	Thr	Leu	Lys	Ser	Glu
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Met	Lys	His	Glu	Asn	Glu	Ala	Leu	Trp	Arg	Glu	Val	Ala	Ser	Leu	Arg
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Gln	Lys	His	Ala	Gln	Gln	Gln	Lys	Val	Val	Asn	Lys	Leu	Ile	Gln	Phe
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Ser	Ala	Pro	Ser	Pro	Ala	Tyr	Ser	Ser	Ser	Ser	Leu	Tyr	Ala	Pro	Asp
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Pro	Ala	Ser	Pro	Met	Ala	Ser	Pro	Gly	Gly	Ser	Ile	Asp	Glu	Arg	Pro
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40

8 40

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Gly	His	Thr	Asp	Thr	Glu	Gly	Arg	Pro	Pro	Ser	Pro	Pro	Pro	Thr	Ser
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Gly	Ser	Tyr	Phe	Ser	Glu	Gly	Asp	Gly	Phe	Ala	Glu	Asp	Pro	Thr	Ile
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Ser

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 that binds with a heat shock transcription factor
 to stimulate gene expression

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41